```
 > O <
 O| |O  Intelligenetics
 > O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-778-187b-1.res made by jdelaval on Fri 17 Jan 103 13:24:27-PST.

Query sequence being compared:US-09-778-187B-1 (1-1598)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-778-187B-1 (1-1598) with:
File : 09-944907.seq

```
100-
    .
    .
    .
    .
    .
 50-
    .
    .
    .
    .
    .
 10-
    .
  5-
    .
    .
    .
    .
  0 -------------------------------------------------*---
SCORE 0   149  298  448  597  746  895  1045  1194  1343
STDEV
SCORE 0
STDEV
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-09-944-907-60	Sequence 60, Application US/09944907	1413	1343	1400	0.00	0

1. US-09-778-187B-1 (1-1598)
   US-09-944-907-60 Sequence 60, Application US/09944907

```
Scores:                    Mean        Median
                           1343        0

                     SEARCH STATISTICS

Randomization group                             0
Cutoff score                                    0
Gap size penalty         0.33                   0
Gap penalty              1.00                   0
Mismatch penalty         1                      0
Similarity matrix    Unitary

                       PARAMETERS
                                     K-tuple          4
                                     Joining penalty  30.
                                     Window size      32.

Times:              CPU              Total Elapsed
              00:00:00.00            00:00:00.00

Number of residues:                  1413
Number of sequences searched:           1
Number of scores above cutoff:          1

Scores:             Standard Deviation
                         0.00
```

Sequence 60, Application US/09944907
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,907
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 60
LENGTH: 1413
TYPE: DNA
ORGANISM: Homo Sapien

```
Initial Score     =  1343   Optimized Score      =  1400   Significance  =  0.00
Residue Identity  =  99%    Matches              =  1404   Mismatches    =  3
Gaps              =  7      Conservative Substitutions  =  0
```

```
            10        20        30        40        50        60
 X   GCG-GCCGCGCCCGACAATGGCGAGTGTAGTGCCTGCCGAGCGGGATCCCAGTGTGCGGCGCAAGCGCG
     |||   | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 CGGACGCGTGGGGTGCCCGACAATGGCGAGTGTAGTGCCTGCCGAGCGGGATCCCAGTGTGCGGCGCAGCGCG
 X   10        20        30        40        50        60        70

            70        80        90       100       110       120       130
 GCGGGGGGCGCGCCTCCCGGGGCTCCGGGTTCGCGTGTTGGCCTTCTCCGCGGCGGCCGCACTGATCCCCACA
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 GCGGCGGGCGGGCCTCCCC-------GGCTCCGGGCGTTCTGCTGTTTGCTTCTTCTCCGCGGCGGCCGCACTGATCCCCACA
            80        90       100       110       120       130

           140       150       160       170       180       190       200
 GGTGATGGGCAGAAATCTGTTTTACGAAAGACGTGACAGTGATCGAGGGAGAGGTTCGGACCATCAGTTGCCAA
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 GGTGATGGGCAGAAATCTGTTTTACGAAAGACGTGACAGTGATCGAGGGAGAGGTTCGGACCATCAGTTGCCAA
           150       160       170       180       190       200       210

           220       230       240       250       260       270       280
 GTCAATAAAGAGAGTGACGACTCTGTGATTCAGCTACTGACTCCAACACAGGCAGACCAGATTTATTTCAGGGAGACTTC
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 GTCAATAAAGAGAGTGACGACTCTGTGATTCAGCTACTGACTCCAACACAGGCAGACCAGATTTATTTCAGGGAGACTTC
           220       230       240       250       260       270       280

           290       300       310       320       330       340       350
 AGGGCCTTTGAAGGACAGCAGCAGGTTTCAGTTGCTGAATTTTTCTAGCAGTGAACTGAACTCAAAGTATCATTGACAAAC
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 AGGGCCTTTGAAGGACAGCAGCAGGTTTCAGTTGCTGAATTTTTCTAGCAGTGAACTCAAAGTATCATTGACAAAC
           290       300       310       320       330       340       350
```

```
360        370        380        390        400        410        420
GTCTCAATTTCTTGATGAAGGAAGGAAGATACTTTTTGCCAGCTCTATACCGATCCCCCACAGGAGAAAGTTACACCACC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GTCTCAATTTCTTGATGAAGGAAGGAAGATACTTTTTGCCAGCTCTATACCGATCCCCCACAGGAGAAAGTTACACCACC
360        370        380        390        400        410        420

430        440        450        460        470        480        490
ATCACAGTCCTCGGTCCCACCACGTAAATCTGATTCAGATAATCCAGAAAGACACTGCGGTGGGAAGGTGAGGAG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCACAGTCCTGGTCCCACCACGTAAATCTGATTCAGATAATCCAGAAAGACACTGCGGTGGGAAGGTGAGGAG
430        440        450        460        470        480        490

500        510        520        530        540        550        560        570
ATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCACCAGCGACTACTCAGGTGGTTCAAAAGGGAACACAGAG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCACCAGCGACTACTCAGGTGGTTCAAAAGGGAACACAGAG
500        510        520        530        540        550        560        570

580        590        600        610        620        630        640
CTAAAAGGCAAAATCGGAGGTGGGAAGAGAGTGGTCAGACAATGTACACTGACCAGTCAGCTGATGCTGAAGGTG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CTAAAAGGCAAAATCGGAGGTGGGAAGAGAGTGGTCAGACAATGTACACTGACCAGTCAGCTGATGCTGAAGGTG
580        590        600        610        620        630        640

650        660        670        680        690        700        710
CACAAGGAGGACGGATGGGGGTCCCAGTGATCTGGAGCCACCCTGCGGGTCACTGGAAAACCTGCAGACC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CACAAGGAGGACGGATGGGGGTCCCAGTGATCTGGAGCCACCCTGCGGGTCACTGGAAAACCTGCAGACC
650        660        670        680        690        700        710

720        730        740        750        760        770        780
CAGCCGGTATCTGAGAGTACAGTATAAGCCTCAAAGTGCACATTCAGATGACTTATCCTCTACAAGGCTTAACC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CAGCCGGTATCTGAGAGTACAGTATAAGCCTCAAAGTGCACATTCAGATGACTTATCCTCTACAAGGCTTAACC
720        730        740        750        760        770        780

790        800        810        820        830        840        850
CGGGAAGGGGACGCGCTTGAGTTAACATGTGAAGGCCATCGGGAAGCCCCAGCGCCTGTGATTGGTTAACTTGGGGTG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CGGGAAGGGGACGCGCTTGAGTTAACATGTGAAGGCCATCGGGAAGCCCCAGCGCCTGTGATTGGTTAACTTGGGGTG
790        800        810        820        830        840        850

860        870        880        890        900        910        920        930
AGAGTCGATGATGAAAATGCCTCAAACACGCGTACTGTTCTGGGCCCAACCTGTTCATCAATAACCTAAACAAA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGAGTCGATGATGAAAATGCCTCAAACACGCGTACTGTTCTGGGCCCAACCTGTTCATCAATAACCTAAACAAA
860        870        880        890        900        910        920        930

940        950        960        970        980        990        1000
ACAGATAAATGGTACAATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTATAATGCTGTAT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACAGATAAATGGTACAATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTATAATGCTGTAT
940        950        960        970        980        990        1000

1010       1020       1030       1040       1050       1060       1070
GTATACAGATCCCCCACAACTATCCCTCCTCCCACAACACCACCACCACCACCACCACCACCACCAC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GTATACAGATCCCCCACAACTATCCCTCCTCCCACAACACCACCACCACCACCACCACCACCACCAC
1010       1020       1030       1040       1050       1060       1070

1080       1090       1100       1110       1120       1130       1140
ATCCTTACCATCACAGATTCCCGAGCAGGTGAAGAAGGCTCGATCAGGGCAGTGGATCATGCCCGTGATC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCCTTACCATCACAGATTCCCGAGCAGGTGAAGAAGGCTCGATCAGGGCAGTGGATCATGCCCGTGATC
1080       1090       1100       1110       1120       1130       1140

1150       1160       1170       1180       1190       1200       1210
GGTGGCGTCGTGGCGTGGCGGTGGTTGGTTCGGTTCGCCATGCCTGGTGCTTCATCATTCTGGGGCGCGCTATTTTGCCAGA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GGTGGCGTCGTGGCGTGGCGGTGGTTGGTTCGGTTCGCCATGCCTGGTGCTTCATCATTCTGGGGCGCGCTATTTTGCCAGA
1150       1160       1170       1180       1190       1200       1210
```

```
1220       1230       1240       1250       1260       1270       1280       1290
CAATAAAGGTACATACTTCACTCATGAAGCCAAAAGGAGCCGATGACGAGCAGCACGCAGCACAGCTATAATC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CAATAAAGGTACATACTTCACTCATGAAGCCAAAAGGAGCCGATGACGAGCAGCACGCAGCACAGCTATAATC
1220       1230       1240       1250       1260       1270       1280       1290

1300       1310       1320       1330       1340       1350       1360
AATGCCAGAAGGAGGACGAGAACACTCCCGAAGAAAGAGAAGAGTAGTCAGCCTTTTTTGTTTCA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AATGCCAGAAGGAGGACGAGAACACTCCCGAAGAAAGAGAAGAGTAGTCAGCCTTTTTTGTTTCA
1300       1310       1320       1330       1340       1350       1360

1370       1380       1390       1400    x  1410       1420       1430
ATGAGGTGTCCAACTGGCCCTTATTTTAGATTGGAAAGGTGGAAGGCTTGGGA    x
|||||||||||||||||||||||||||||||||||||||||||||||
ATGAGGTGTCCAACTGGCCCTTATTTTAGATTGGAAAGGTGGAAGGCTTGGGA  x
1370       1380       1390       1400       1410

1440       1450       1460       1470       1480       1490       1500
TTTTTTTATGAATGGGTGGAAAGGTGTGAGACTGGGATTTGCTGTGTAAAAAAAAAAAAAA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TTTTTTTATGAATGGGTGGAAAGGTGTGAGACTGGGATTTGCTGTGTAAAAAAAAAAAAAA
1440       1450       1460       1470       1480       1490       1500

1510       1520       1530       1540       1550       1560       1570
ATGTTCTTTGGAAAGAAAAAGCGGCCCGCTTTCTTATTCTATTTCAACATTCAGCTTAATCATTAAATCCTAAA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATGTTCTTTGGAAAGAAAAAGCGGCCCGCTTTCTTATTCTATTTCAACATTCAGCTTAATCATTAAATCCTAAA
1510       1520       1530       1540       1550       1560       1570

1580       1590
ATCATACATGCTATTTCCAT
1580       1590
```

Fri Jan 17 13:25:13 2003 us-09-778-187b-2.res Page 1

```
> O <
O| |O  Intelligenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-778-187b-2.res made by jdelaval on Fri 17 Jan 103 13:23:42-PST.

Query sequence being compared:US-09-778-187B-2 (1-442)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-778-187B-2 (1-442) with:
File : 09-944907.pep

```
100-
  |
N |
U 50-
M |
B |
E |
R |
  |
O 10-
F |
  |
S 5-
E |
Q |
U |
E |
N |
C 0-
E    |----|----|----|----|----|----|----|----|----|
S    0   47   94  141  188  235  282  329  376  423
SCORE 0                                          *
STDEV 0
```
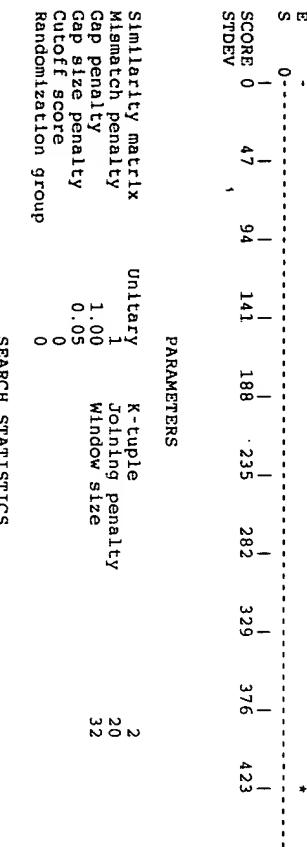
PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	32
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

	Mean	Median
Scores:	423	0

	Standard Deviation
	0.00

Times:
```
     CPU           Total Elapsed
00:00:00.00        00:00:00.00
```

Number of residues: 440
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-09-944-907-61	Sequence 61, Application US/09944907	440	423	439	0.00	0

1. US-09-778-187B-2 (1-442)
   US-09-944-907-61 Sequence 61, Application US/09944907

Sequence 61, Application US/09944907
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,907
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien

Initial Score   =   423   Optimized Score   =   439   Significance   =   0.00
Residue Identity =   99%   Matches   =   440   Mismatches   =   0
Gaps   =   2   Conservative Substitutions =   0

```
              10        20        30        40        50        60        70
X    MASVVLPSGSQCAAAAAAAAAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDS
     |||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
X    MASVVLPSGSQCAAAAAAAAPPG--LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDS
              10        20          30        40        50        60

              80        90        100       110       120       130       140
     VIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPP
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     VIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPP
              80        90        100       110       120       130

              150       160       170       180       190       200       210
     RNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEMSDMYTVTSQLMLKVHKEDDGV
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     RNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEMSDMYTVTSQLMLKVHKEDDGV
              150       160       170       180       190       200       210

              220       230       240       250       260       270       280
     PVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRDDDEMP
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     PVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRDDDEMP
              220       230       240       250       260       270       280

              290       300       310       320       330       340       350
     QHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVVDPPTTIPPPTTTTTTTTTTTTTTTTTTTD
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     QHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVVDPPTTIPPPTTTTTTTTTTTTTTTTTTTD
              290       300       310       320       330       340       350
```

```
        360        370        380        390        400        410        420        430
SRAGEEGSIRAVDHAVIGGVVAVVFAMLCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQN
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SRAGEEGSIRAVDHAVIGGVVAVVFAMLCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQN
        360        370        380        390        400        410        420        430

        440 X
NSEEKKEYFI
||||||||||
NSEEKKEYFI
        440
```